

A. Exon 1

| | | | | | |
|--|---|-------|--------|-------|------|
| BsaI | BseRI | SfI | EarI | | |
| AGCTCAGAGACCCAAAGAGCCGCCCTCACATCACACAGGCTCTCCCGGCCAACGACTGCTGGCTTGGCAACACGCCATACAGGAGAGGGGGGCTGGCGGCCACCGCGT | TGGAGTCTCTGGTTCTCGCGGAGTGTATGTGTCGAGGAGGGCGGGTCTGTGAGCACGCCAACCTGTGGCGGATGTCCTCTCCGCCCGGACCCCCCGGGTGGCGGA | | | | |
| EaeI | BssHII EcoNI | BamHI | SdiI | | |
| GATGGCCGAGGCCGCTCGACCGAGGCTCCGCTATAAAGTCGAGCCCGCTGGTCCCTACGCCAGACGTTCTGCCCGAGAUTGCCCGGTTCTGCTTCACAGTGTGTTGA | | | | | |
| CTAACCGCCCTCGCCGCGACTCGCTCTGGCGATATTACGCCGGGGGACCAAGGATGCGGTCTGAGAGCGGGTCTCACSGCCGCCAACAGACGAAAGTTGCAAACT | | | | | |
| BsiHKAI | PshAI | EagI | Bpu10I | BamII | BpmI |
| ACGGAAACCGGTGCTCGACCCCTCGACCCCGCTCGGCGCCTTGAAGCTGAGCCCTTGCAACTCTGTCGCTCCCGGCTCAGCGTCGCCCTCGGCCCTGTCGAGCCCG | | | | | |
| TGCCCTGGGCCAGAGCTGGGAAGGCTGGGGCAAGCCCGGAAACTCGGAACTCGGAAACGTTGAGCAGCGAGGCGGGAGUTCGCAGCGGAGGCCGGAGCGGTGGCGG | | | | | |
| DrdI | BspHI | BsmBI | | BpmI | Ncol |
| ATCATGACCAACGGCGTCCCTCGAAGTGCCTCCAGAAACTACACCAAGGACTCGAGGCTGCCATCACCGGCCAGATCACTGATGCTCTTACGCTATCTGTC | | | | | |
| TAGTAGCTGGCGCAGAGGAGCCTTACGGGCTTGTGTTGTCGACCTCCGACGCTGTTGGGGCTAGTTGGACCTCAACATACCGAAGATCAGATGACAGG | | | | | |
| ► Met1 Thr1 Thr1a Ser1 Pro1 Ser1 Glu1 Val1 Arg1 Glu1 Asp1 Tyr1 His1 Glu1 Asp1 Ser1 Glu1 Ala1 Ala1 Leu1 Asn1 Arg1 Glu1 Ile1 Asn1 Leu1 Glu1 Leu1 Tyr1 Ala1 Ser1 Tyr1 Val1 Tyr1 Leu1 Ser1 | | | | | |
| Drall | | | | | |
| StyI | Adel | | | | |
| ATGGTGAGTGCGGCCCTGGCTTTCGCGGGGCCAAGAGAGGTTGGCCCTGGCTCCCTGGGCCACTTGGTAGGCTGGCGAGGGTGGGTTGGGGCTGGCTGGCGG | | | | | |
| TACCACTCACGCCGGACCGGAAACGCCCGCCCTTCTCCACGCCGGACCGGAGGAAACCCGGTGAACCAACTCGACCCGCTCCACCCACCCGACGCC | | | | | |
| ► Met1 | | | | | |

B. Exon 2

GCATCTGCCTGCTGCGGATCAATAACAACTACCCCTTCCACTTCACTCTTCACTCTGTTATTTGACCGGGATGATGCTGCGCCCTGAAAGAACTTGCACAAATACTTTCTCCATCAACT
 CGTAGACGUACGACACCCCTAATTATTGTTATGGGAAAGGUAAAGCTCAGAACATGAAACCTGCGCCCTACTACACCGGGACTCTCTGAAACGGTTATGAAAGAGGTAGTTAGA
 ▶ Ser CysTyr PheAspPar GaspAspValAlaLeuLysAsnPheAlaLysTyr PheLeuHisGlnSer

C. Exons 3 and 4

PstI Afill BsmI BsrBI BsmI BsrDI ApaI BsgI
 CTGCAAGATGAAATTGACATGTTCTTGATTCTGAAACCTGACCGTGAATGAGCTGGGCTGAACTGAGATGTTGCACTGGCATTGGGAAAGAGTGTGAATCAGTC
 GACGTCTACTTAACTGTAACAAAGAAACTAAGTCTTGGACTGGCACTACTGACCTCTCGGCCGACTTACGTTACTCCACAGTGACGTGAACTTTCTCACACTTACTGAGT
 ▶ LysPr oAspAr gAspAspTr pGluSer GlyLeuAsnAlaMeIaFrgyOsAlaleuHiSLeuGlyuLysSerValAsnGlnSer
 Pml Drai
 CTACTGGAACTTCACAAACTGGCTACTGACAAAGAATGATGATCCTTACGAACTGAGATCATGAAACGGGCTGAGTGGAGATGATTGGCACAGGGCTGGGAGAGCTGACCACTAACCG
 GATGACCTTGAGATGTTGACCGATGACTGTCTTAACTAGGGGTGACTCTAGCTCTTGTGCCCCACTCACCTCTACTAAACGGTGTCCCGAACCCCTCTGCACTGGTCATTGG
 ▶ LeuLeuGluLeuHiSLeuAlaThrAspLysAsnAspProIaHis
 BsmBI BspMI XcmI BsmI BsiEII Pml
 CTGTCCCCATGTTCTCTTCTAGTTATGTGACTTCATTGAGACGCATTACCTGAATGAGCAGGTAAATCCATTAAAGAACCTGGTGCACCACTTACGCCRAAGATGG
 GACAGGGTACAGAGAAAGGTCAATACACTGAGACTCTGGCTTAATGGACTTACGTCCTTAACTTGGTAATTCTTGACCCACTGGTGTGACTGGTTGAATGCGTTCTACC
 ▶ LeuOsPheIleIleIuThrHiSThrLeuAsnGluGluNlysLysIleuGlyAspHisValThrAsnLeuArglysMeIIG
 BanII MsII SphI AaII Sty I BstAF
 GAGCCCCCTGAATCTGGCATGGCAGAATATCTCTTGACRAAGCACACCCCTGGGACACGGGTGATGAGAGCTAAAGCTGACGCCAAAGGCATGTGACTTTACTGGCTCACTGAGG
 CTCGGGGACTTAGACCGTACCCCTTATAGAGAAAATCTGTCTGTTGACCCCTGTGCACTACTCTCTGATTGACTGCAAGGGTTCCGGTACACTGAAATGACCGAGTGAATCC
 ▶ IaIaIaPr oGluSer GlyMeIaIaGluTyrLeuPheAspLysHiSThrLeuGlyHiSglyAspGluSer...
 Ppu10I Xapi
 Nsi Apol
 EcoT22I KpnI
 SphI AcsI
 CAGTCATGATGTCAGGCTGCCATTATCTTCTATAAGTGCACCAAAACATCTGTTAAAGTCTTAACTTGTACCAATTCTCAAAATAAGAATTGGTACCCAGCT
 GTCACGTACGTACGTCGACCGAAATAGAAAAGTATTCAACGTTGGTTGTAGACGAAATTTCAGAAATAATCAGTAAAGAATTTTCTTAAACCATGGTCA
 ▶ SspI
 CTTGTTGTGATTGAGGATGAGCGCACCAGCTTCCCTGCGTCGGCTATATAACCAACTGCAACGGCTGAAAGAATATTATAAACTCTGTAATTGGGAAAGATAGTGAAGAAG
 GAACAAACACTTAACTCCGCTGGTCAAGGGAAACGACGGCATATAATGGTGTGACGTTGGCAGACTTCTTATAAAATAATTGAGCATCAACCCCTTCTACACTTCT
 DseI Sty I
 DrdI BspMI NcoI XmnI SmlI
 CAGGGTGTGTCAGACAGGAACTAAGCAGTCAGTCTGGTCTGAGTTACCTGGCAGACTGCCATGGAAACATATTCTGAGTGT
 GTGCCACACAGTCCTCTGATTCGTCAGGACAAAGACTCAATGGACGCTCTGACGGTACCCCTGTGAAAGACTCACAG

FIGURE 1

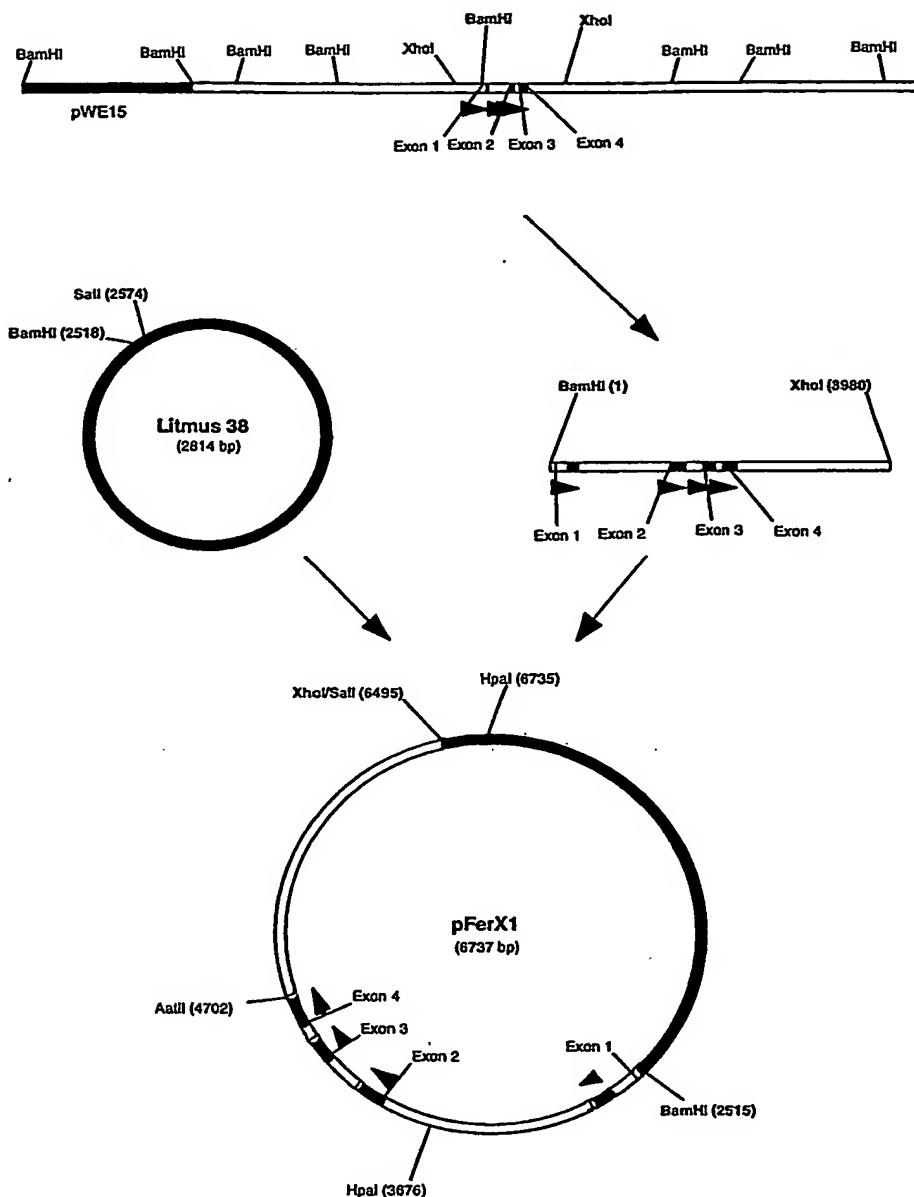


FIGURE 2

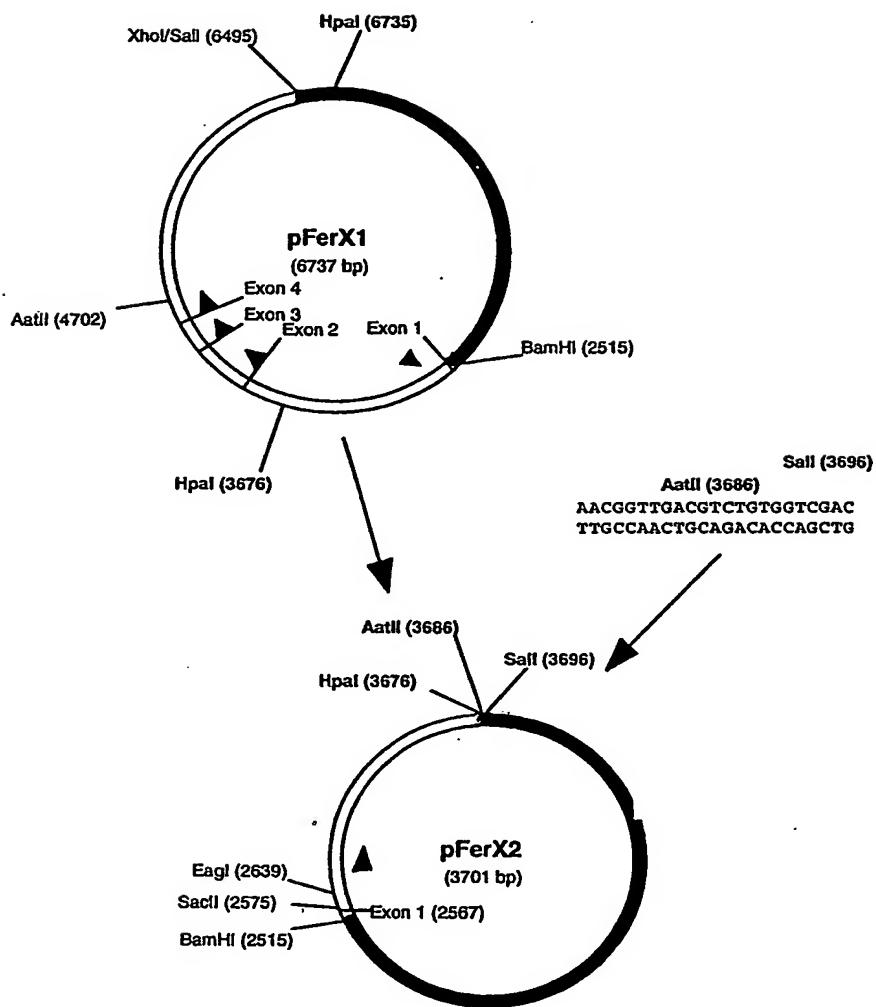


FIGURE 3

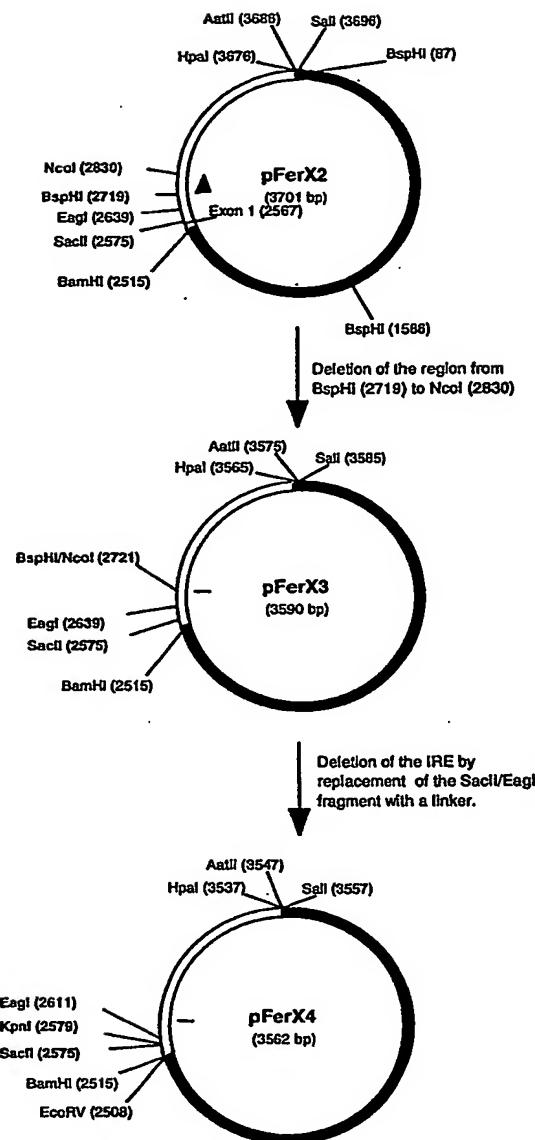


FIGURE 4

A

B.

9er1
 ATC TGT CCA TG GTGAGTGC~~GG~~CTGGC~~GG~~CTGGC~~GG~~GGAAAGAGGGTGC~~GG~~CTGGC~~GG~~CTGGC~~GG~~ACTTGGTGA~~GG~~CTGGC~~GG~~AGGG

 TGGGTTGGGGCGTGGCTGCGGCTTCCCCGCTTCCAGCGCCCTTCTGAAAATGGAGTTGTCCGGGGTCTTCCAAAGGCAGG~~AG~~CCCT
 GCGCTGGCAAGTCTGAGCACTAGCGCTTGTGCTCTGCATAGAC~~CC~~AGG~~AC~~GT~~AT~~AAACCCGT~~TT~~TGAGCCTT~~AG~~GGCTG~~TA~~CAACTG~~T~~
 CAGCCTCCAA~~CT~~CAACCC~~T~~GCAGTTAGGTG~~C~~ATTTCTGC~~ACT~~CTG~~CC~~CTC~~GG~~T~~C~~AC~~AT~~GGC~~CT~~TG~~AG~~GG~~CT~~TCTGTTGGGT~~TA~~CTC
 CAGCTCCAGTTCTCTG~~ACT~~ATGGCGGGTCTGCTTGGT~~C~~ATGGT~~G~~GAATGGCAGG~~CC~~CTGGGG~~CT~~TGGT~~AC~~AAAGAGG~~CT~~TATCTCTGT~~GA~~ACTT
 ACTCTAA~~CC~~ACTTGT~~GA~~AGCAGCG~~GG~~CT~~AC~~ATCT~~CT~~GC~~TT~~ATCACAG~~GC~~CT~~AC~~TTG~~C~~AT~~GA~~AACTTATCGT~~GA~~AGG~~AT~~CTCC~~CC~~CTCTGT~~AA~~
 TCACCC~~T~~GC~~AC~~CTT~~GC~~CAAGGC~~T~~CTAGAGTACTGTAC~~G~~TTT~~T~~TTTG~~C~~AC~~AG~~TGT~~G~~CTT~~AC~~T~~CA~~AGAAGTAGT~~G~~GTAA~~CA~~T~~AC~~
 TTGGT~~G~~AAAAG~~CC~~ACGG~~TT~~GGG~~AAA~~AC~~AT~~T~~AT~~GT~~GA~~AA~~TA~~CAA~~TA~~AC~~AT~~GT~~G~~CT~~AA~~ACTG~~AA~~AT~~CA~~AGC~~CT~~TC~~CC~~AA~~AT~~GT~~AA~~

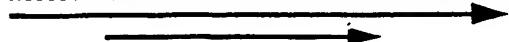
 TTGTGCT~~AA~~ATAC~~AT~~GC~~CC~~TCAG~~TT~~AA~~CC~~AG~~GT~~TA~~TC~~AGCAG~~TT~~GG~~CT~~GT~~CT~~AG~~CT~~G~~AA~~AC~~CT~~T~~G~~AGAC~~CT~~T~~G~~T~~TA~~AC~~CC~~AT~~TT~~TT~~TT~~TT
 TT~~TA~~AC~~AT~~GATTGT~~G~~GAAGGAGAGAAT~~T~~GAC~~CT~~CC~~CA~~AT~~G~~AGGG~~CA~~T~~T~~AG~~CC~~CCCC~~CC~~T~~C~~CA~~G~~AA~~AA~~AT~~GA~~AT~~T~~GG~~CT~~GG~~CT~~AA~~AG~~TT
 TT~~TC~~T~~CT~~GC~~AC~~TA~~AT~~T~~GG~~GAG~~CC~~AT~~GA~~AA~~CC~~CT~~T~~G~~AT~~AA~~AG~~CC~~AA~~GT~~CC~~AA~~GT~~T~~GT~~TT~~CC~~AT~~CT~~TA~~CT~~TT~~AA~~AG~~GC~~CA~~GT~~GG~~GT~~AC~~AR~~
 SW~~8-2~~ No~~1~~ FN~~2~~
 ACAGC~~CT~~TTAC~~AC~~CCATTG~~C~~AT~~T~~GC~~CT~~T~~G~~CT~~GG~~GT~~CA~~AT~~A~~AC~~AA~~AT~~CC~~CT~~CC~~ACT~~T~~TCAG~~CT~~G~~TA~~GG~~CC~~GG~~CT~~G~~AC~~GT


FIGURE 5A

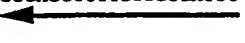
C.

FN1 Swa-1 NolI AatII

ACTTTCAGCTGCTAGCGGCCGCGCTGACGTCCCCAAGGCCATGTGACTTTACTGGTCACTGAGGCAGTGCATGCATGTCAGGCTGCCCTTATCTTT



TCTATAAGTTGACCAAAACATCTGCTTAAAGTTCTTAATTGTACCAATTCTCAAAATTTGACGCTCTTGGTACCCAGCTCTGGTGTGATTG

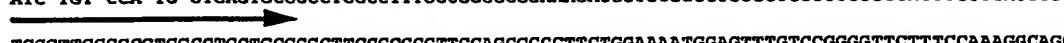


Fer4

D.

Fer1

ATC TGT CCA TG GTGAGTGCGGCCCTGGCTTGGCGGGCGGAAAGAGGGTGCGCCCTGGCCACTTGGTGAAGCTGGCGAGGG



TGGGTTGGGCGTGGCCCTGCGGGCTTCCCGCCTTCCAGCGCCCTTCTGGAAAATGGAGTTGTCGGGGGTTCTTCCAAAGGCAGGCAGCCCT

GCCGTTGCAAGTCTGAGCCTAGCGTTGTGGCTCTGCATAGACCCAGGCAGTCATAACACCCGTTGGCTTGAAGCCTTAGGGCTGTACACT

CAGCCTCTCAATCAACCCCTGAGTTAGGTGATTTCTGCACACTCTGCTCCCTCCGGTCACATGGCCTGAGGCTTCTGTGTTGGTGTACATC

CAGCTCCAGTTCTCTGACTATGGCGGTCTGCTGATGGTGTGAAATGGCAGCCTGGGCTTGGTACAAAGAGGGTTATCTCTGTGAAACTT

ACTCTAACCACTTCTGAAGCAGCCTACATCTGCTTATCACAGGCCCTCAGTCATTGAAACTTATCGTAGGAATCTCCCTTCTGTA

TCACCCCTGACCTTGCAAGGCATCTAGAGTACTGTACGTTTAATTTTTATTGACCAAGTTGTCCTACTAACAGAAGTAGTAGGTAACTAC

TTGGGAAAGGCCACGGTGGAAAAACATTATCGTGAATACAAACTGAGTGCTAAACTGARAATCAAGCTTCTCCAAATGTAT

HpaI

TTGTGCTAAATACAATGCCCTCAGTTAACCAAGGTAATCAGCAGTTGGCTGTCTAGCTGAAACCTTGAGACCTTGTGTTAACCACTTTTTA

TTAACATGATTGTTGAAGGGAGAAATTGACCTCCAAATGTAGGGCATTAGCACCCCCCTCTCACAGACAATAGATAATGCCCTGGCTTAAAGTT

TTTCTGCACTAATGTGGAGCCATAGAACCCCTTGATAAAAGCCAAGTCCCAAGTTGTTTCCATCTTAAAGGCCAAGTAGGGTGACAA

Swa-1 Swa-2 NolI AatII

ACAGCCTTACCAACATTGCATCTGCCCTGCTGTGGGATCAATAACAAATACCCCTTCCATTAAATCTGCTAGCGGCCGCTGACGCTCCCCAAGGC



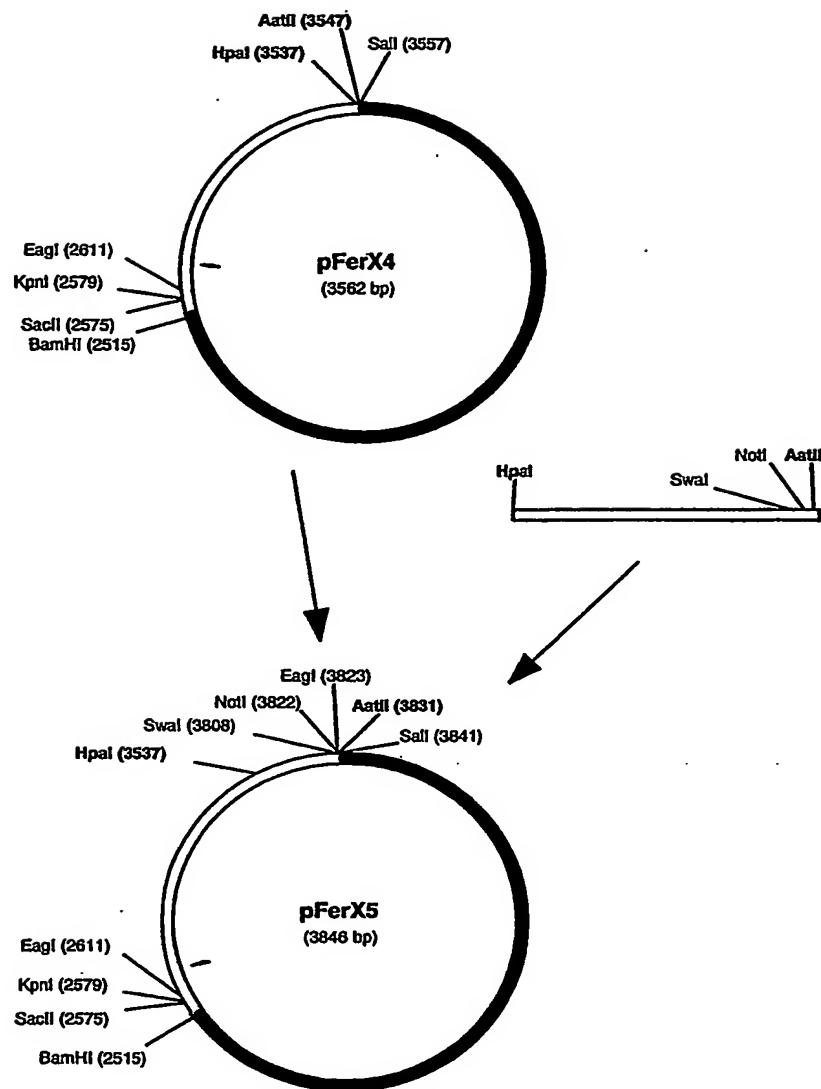
CATGTGACTTTACTGGTCACTGAGGCAGTGCATGTCAGGCTGCCCTTATCTTTCTATAAGTTGACCAAAACATCTGCTTAAAGTTCTTA

Fer4

ATTTGTACCAATTCTCAAAATTTGACGCTCTGGTACCCAGCTTGTGATTG



FIGURE 5 B

**FIGURE 6**

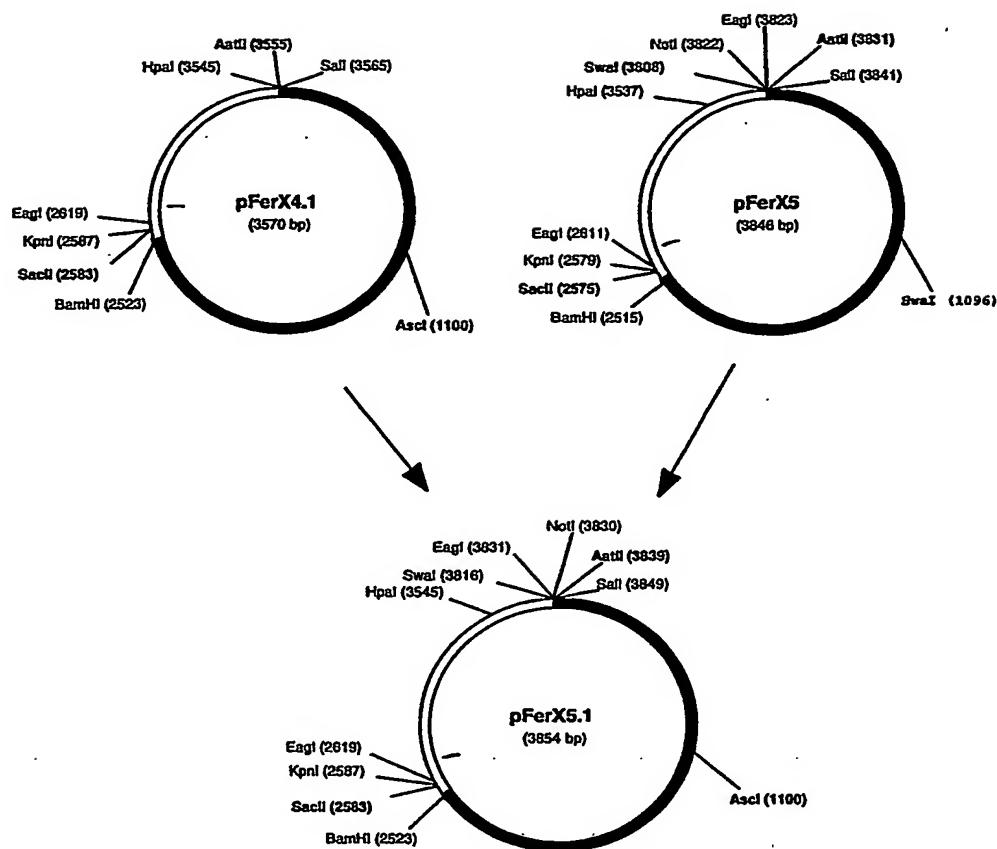
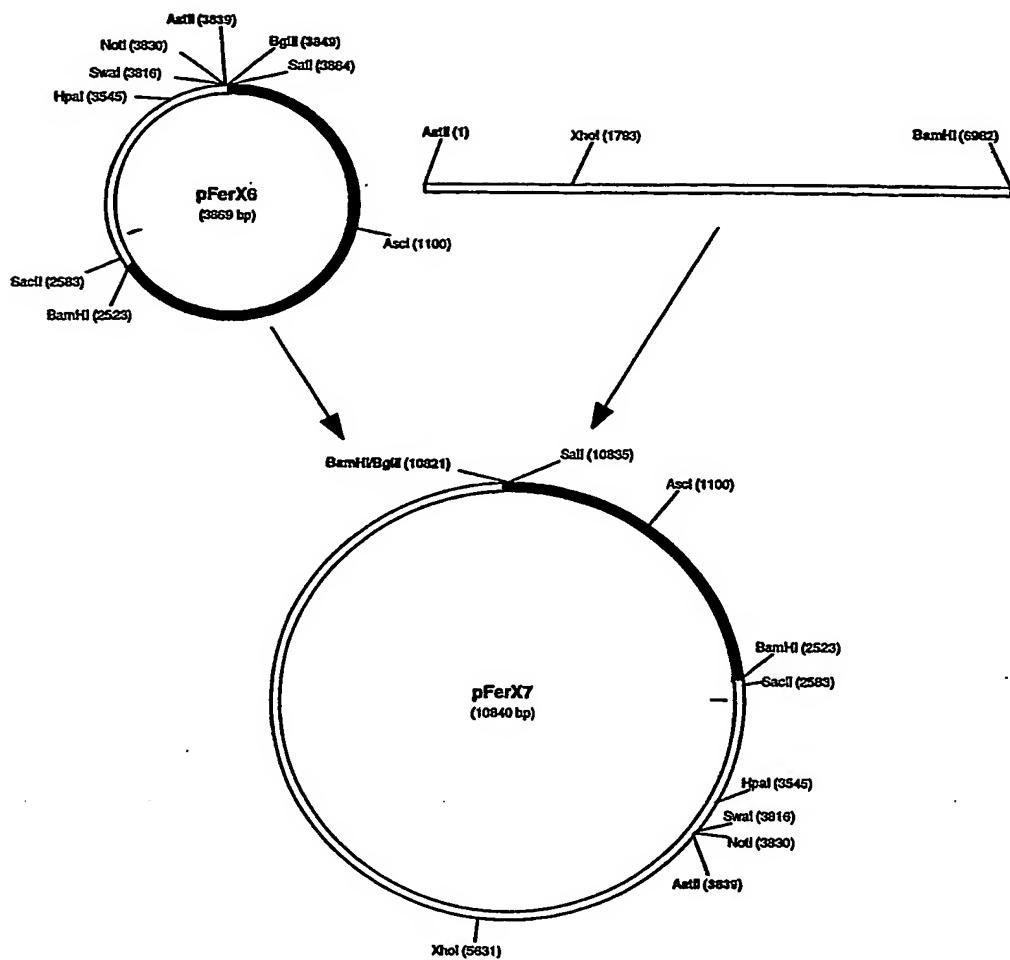


FIGURE 7

**FIGURE 8**

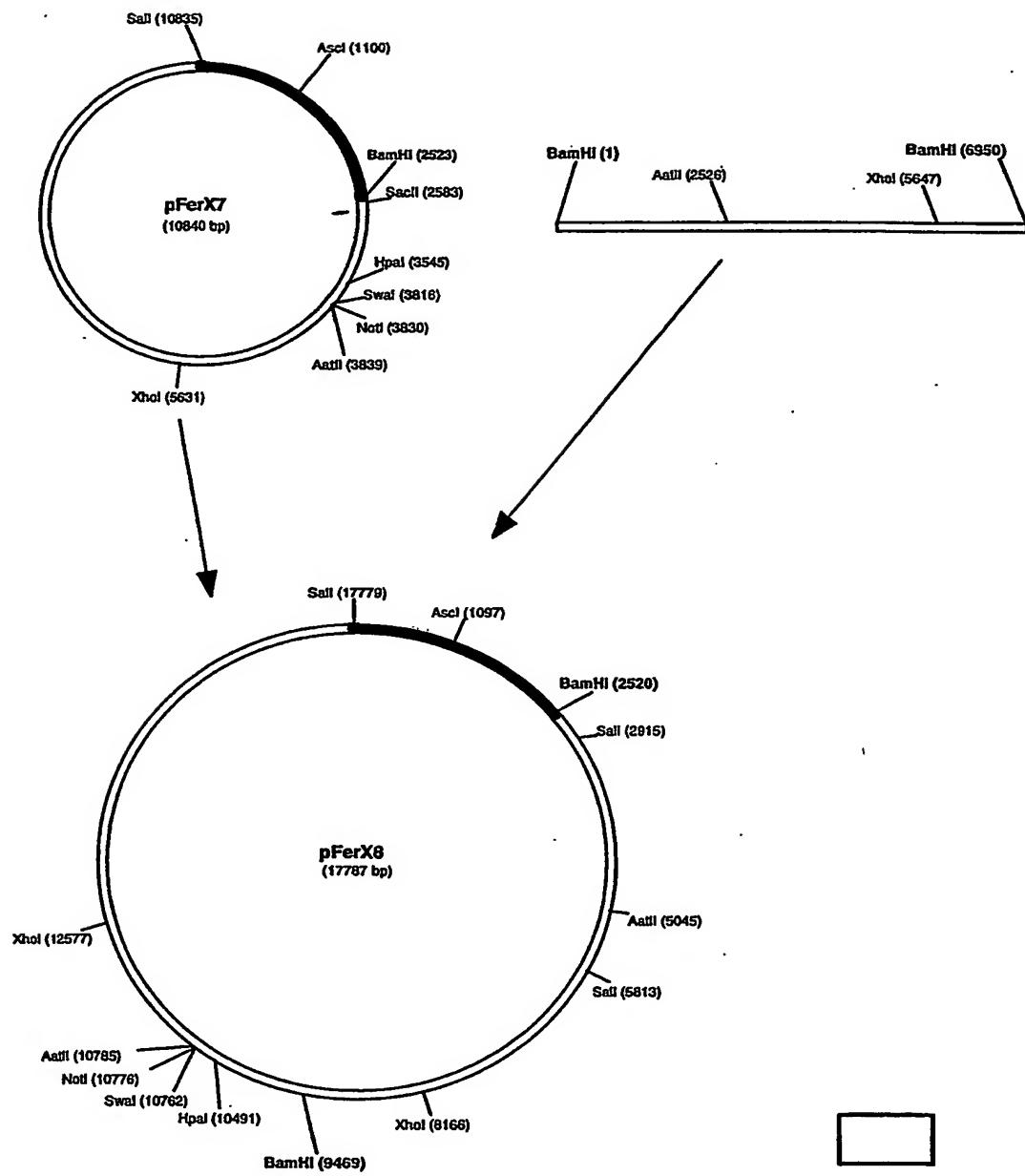


FIGURE 9

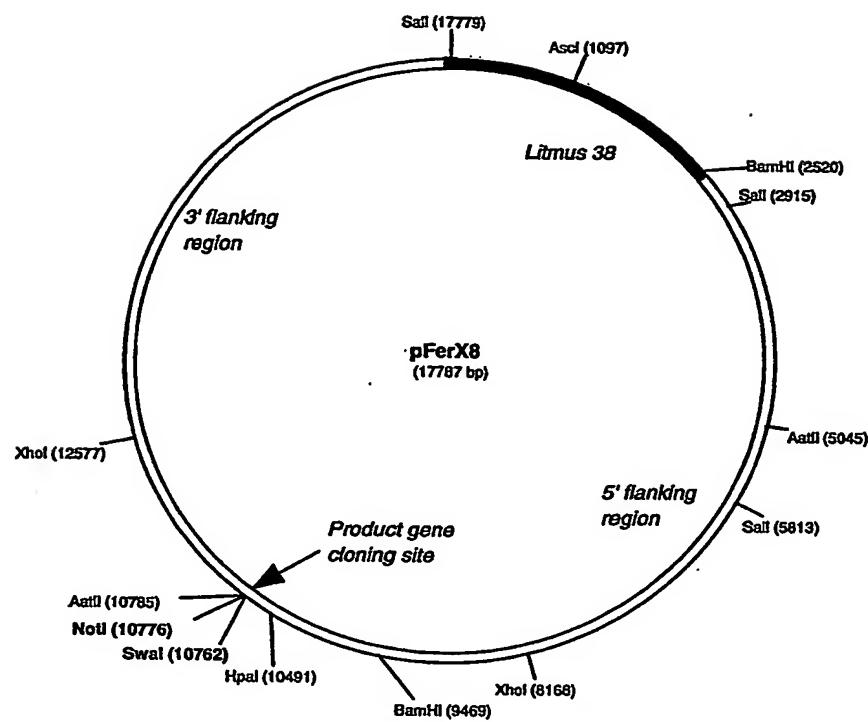


FIGURE 10

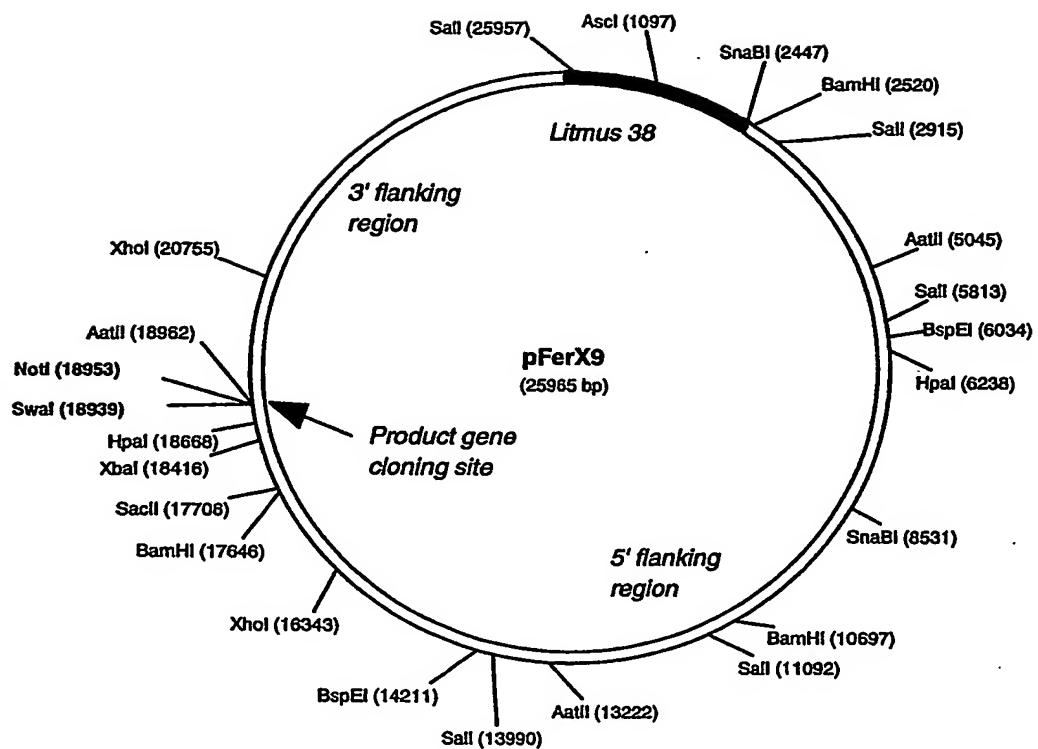


FIGURE 11

SacII

BamHI (9469)
GGATCCCGCTATAAAGTGCGGCCCCGCTGGTCCCTACGCCAGACGTTCTCGCCCAGAGTCGCCGGTACCGGTGCTCG
 ACCCCTCCGACCCCCGTCGGCCGCTTGAGCCTGAGCCCTTGCAACTCGCTCCGCCGCTCCAGCGTCGCCCTC
 CGCGCCTCGCCCAGGCCATC ATG gtgagtgcggcctggccttggggggggaaagagggtgcggcctggcct
 ▶ Met

cccttggccacttggtagctggcgagggtgggtggggcgtggcctgtgcgggcttccccgcctccagcgccc
 ttctggaaaatggagttgtccgggttcttccaaaggcaggcagccctgcgtggcaagtctgagcacctagcgct
 ttgtggctctgcataagaccaggcacgtcataacaccgtgtttgaagccttagggctgtacaactgtcagcctctc
 caatcaaccctgcagttagtgcatttcctgcactctcgcccccccggtcacatggcctgcaggctctgtttg
 ggtgtacatccagctccagttcctctgactatggcggtctgttggcatgggtggaaatggcagccctgggctg
 gtacaagaggcttatctttgtgaacttactctaaccacttctgaagcagcggccttacatctctgttacacag
 agcctcacttgcattgaaacttatcgctaggaatctcccttctgtaatcaccctgaccttgcacaggcatctagagt
 actgtacgttttaattttatttgcaccagttgttactaacagaagttagtagtaacataacttggaaaa
 agccacggttggaaaaaccattatcgtaatacaaataactgagtgcctaaaactgaaaatcaaagcttctcc
 caatgtatttgcataaaatacaatgcctcagttcttaaccaggtaatcagcagttggctgttagctgaaaacctt
 gagaccttgcgttaaccatttttatttaacatgattgtgaaggagagaattgacccatgtggagccatagaacc
 cttgataaagccaagtcccaagttgtttccatccttactttaaaggccaagttagggtgacaaacagccttacca

AatII (10785)

Swal (10762) **NotI (10776)**

ccattgcattgccttgcgtggggatcaataacaaataccctttccatttAAATCTGCTAGCGGCCGCTGACGTCCC
 CAAGGCCATGTGACTTTACTGGCACTGAGGCAGTCATGCATGTCAGGCTGCCTTATCTTCTATAAGTTGCACC

KpnI (10927)

AAAACATCTGCTTAAAGTTCTTAATTGTACCATTTCTTCAAAAATAAAGAATTGGTACCCAGCTTTGTTGTGAT
 TGAGGATGAGCGCACCAAGCTCCCTGCGCTATACTAACACACTGCA

FIGURE 12

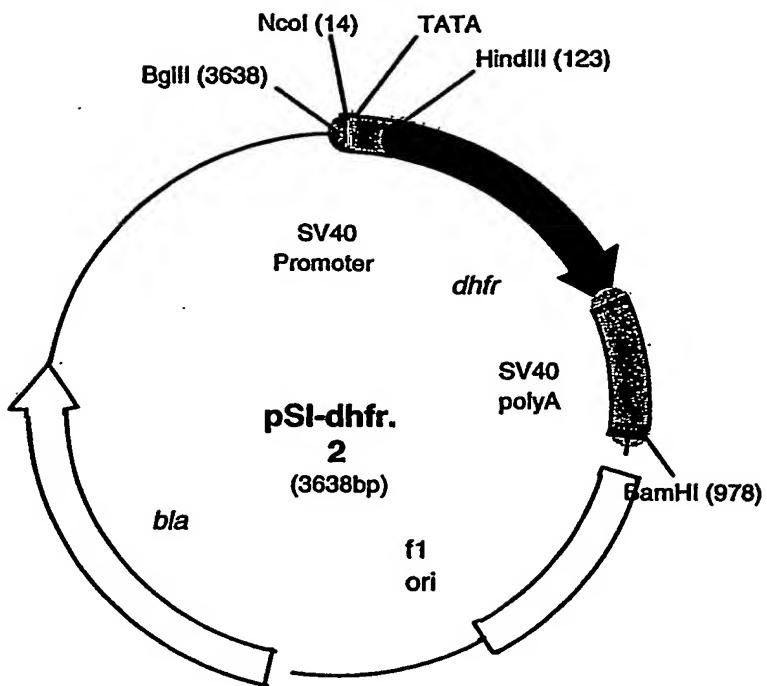
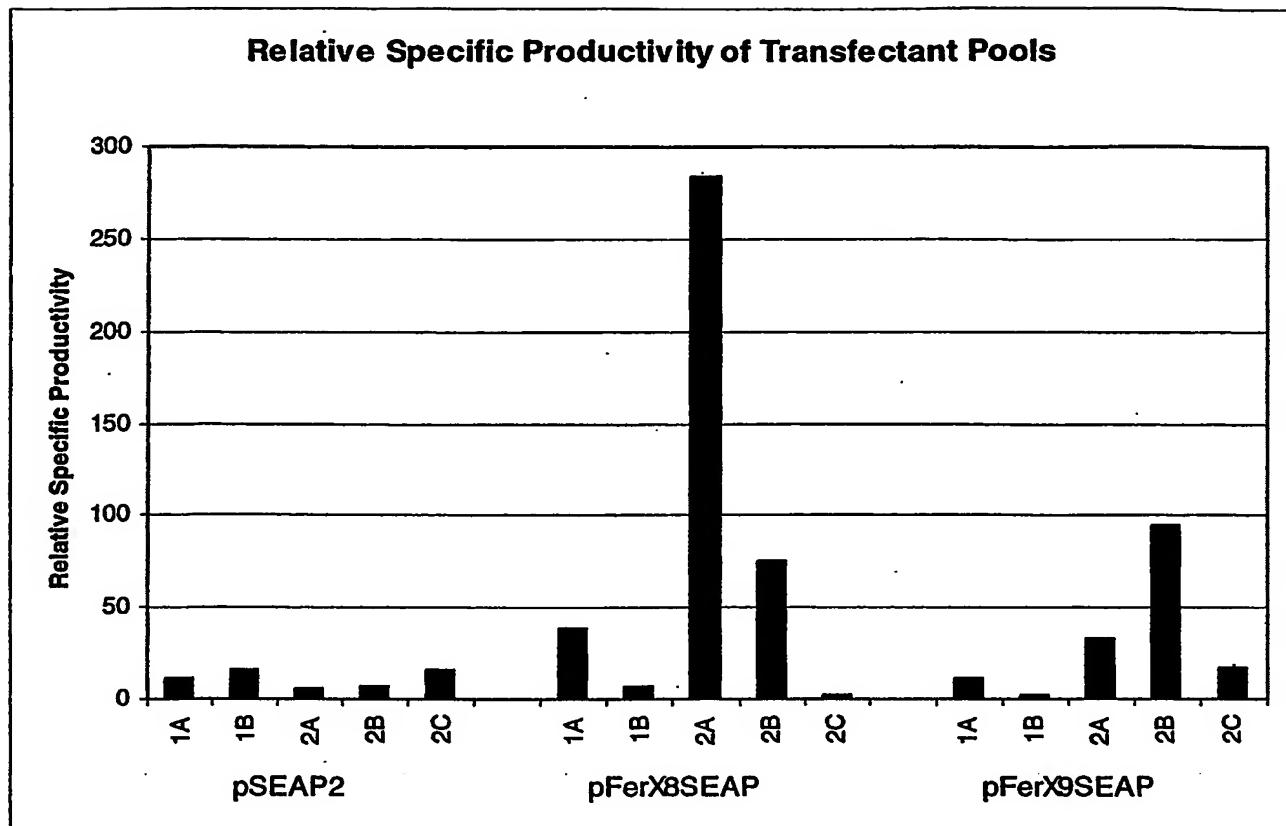


FIGURE 13

**FIGURE 14**

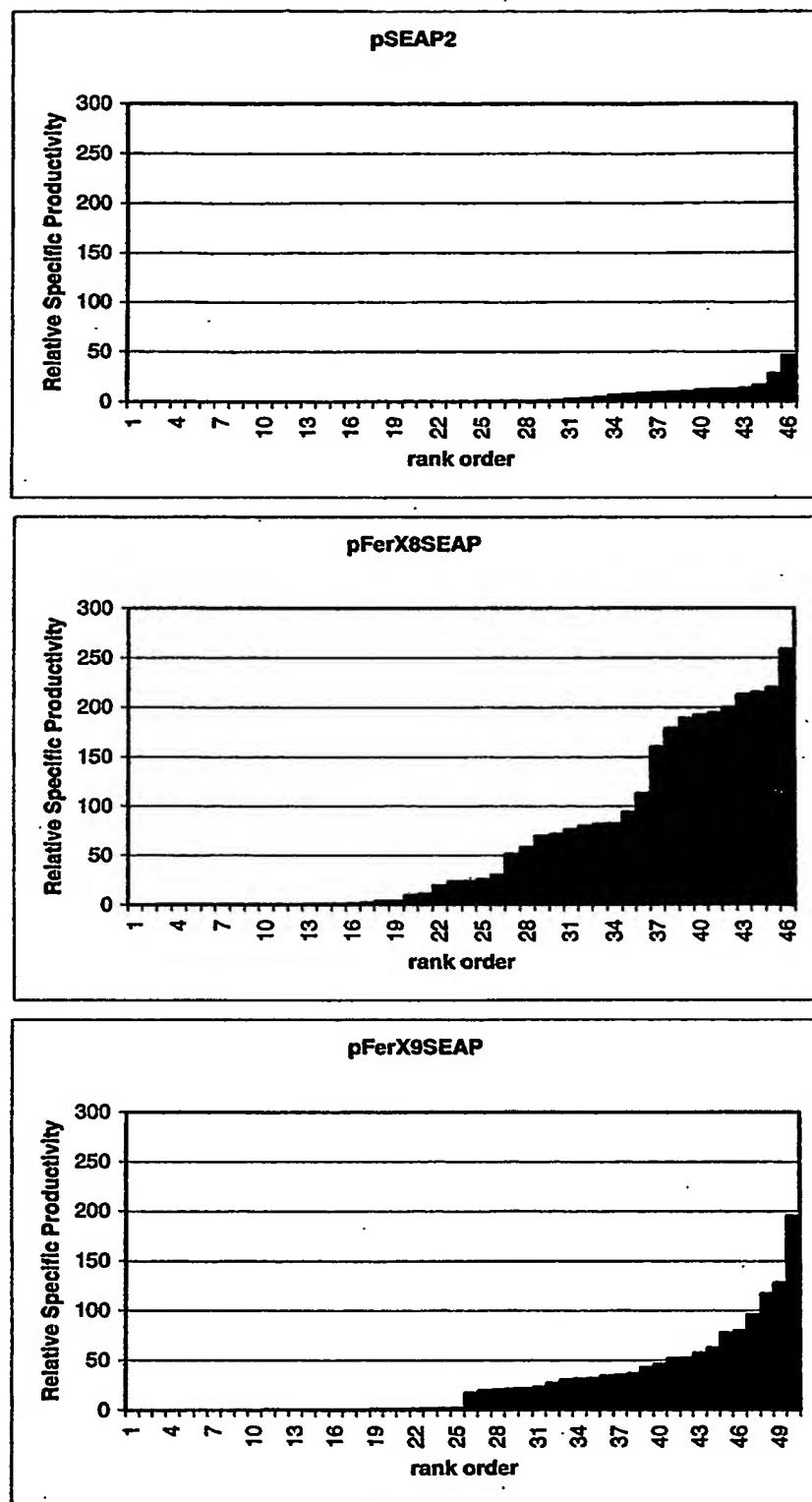


FIGURE 15